

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 26, 2002, 20:33:06 ; Search time 1934 Seconds

(without alignments)  
4836.293 Million cell updates/sec

Title: US-09-840-795-18\_COPY\_78\_770

Perfect score: 693

Sequence: 1 atgagttgcacgaagaatga.....agcagcaggggcctgaatg 693

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## ALIGNMENTS

18	76.6	11.1	401	9	AA003356	AA003356 mg49501.r
19	71.8	10.4	526	9	BB856841	BB856841 BB856841
20	67.7	9.7	358	9	AA036247	AA036247 ml74803.r
21	64.4	9.3	499	9	BB858206	BB858206 BB858206
22	60.2	8.7	678	9	BB641271	BB641271 BB641271
23	59.6	8.6	673	10	B1904967	B1904967 603169073
24	58.2	8.4	1110	12	CNS0507C	AL347097 Tetradodon
25	57	8.2	626	9	BB652914	BB652914 BB652914
26	52.4	7.6	275	9	AV111112	AV111112 AV111112
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28	46	6.6	612	12	AQ021525	AQ021525 CIT-HSP-2
29	42.2	6.1	670	10	B1253347	B1253347 602973621
30	39.6	5.7	708	9	AL655137	AL655137 AL655137
31	39.2	5.7	803	9	AL569968	AL569968 AL569968
32	38.6	5.6	547	10	BG897869	BG897869 HOAI-1-84
33	38.6	5.6	568	10	BM010615	BM010615 603631828
34	38.6	5.6	641	10	BE276747	BE276747 601178305
35	38.6	5.6	706	9	AL580892	AL580892 AL580892
36	38.6	5.6	713	10	BG752816	BG752816 602732651
37	38.6	5.6	817	10	BG575868	BG575868 602598686
38	38.6	5.6	884	10	BG696700	BG696700 602659716
39	38.6	5.6	889	10	B1522640	B1522640 603175660
40	38.6	5.6	939	10	B1520358	B1520358 603071833
41	38.6	5.6	970	9	AL551177	AL551177 AL551177
42	38.6	5.6	1048	10	BM458980	BM458980 AGENCOURT
43	38.6	5.6	1067	10	BF037815	BF037815 601461984
44	38.6	5.6	1096	10	BG391978	BG391978 602409924
45	38.6	5.6	1176	10	B1911227	B1911227 603062988

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	403.2	58.2	689	9	BB219800 BB219800
2	362.2	52.3	951	10	BM013263 603635039
3	359.2	51.8	697	9	BB627119 BB627119
4	327.8	47.3	680	9	BB651661 BB651661
5	291	42.0	614	9	BB637179 BB637179
6	186.8	27.0	459	9	BB858916 BB858916
7	169.6	24.5	442	10	BE554624 BE554624
8	148.2	21.4	680	9	BB663265 BB663265
9	135	19.5	616	9	BB650696 BB650696
10	133.2	19.2	395	10	BE306459 601103459
11	122.4	17.7	589	10	BJ0004238 BJ0004238
12	110.4	15.9	894	10	BF162288 BF162288
13	100.6	14.5	932	10	BT1919139 BT1919139
14	94	13.6	519	9	BB857078 BB857078
15	91.4	13.2	534	10	BE757704 212225 MA
16	86	12.4	566	10	BC835626 354836 MA
17	79.2	11.4	258	9	BB542020 BB542020

TITLE  
JOURNAL  
COMMENT

RESULT 1  
LOCUS BB219800  
DEFINITION BB219800 RIKEN full-length enriched, adult male aorta and vein mus  
musculus cDNA clone A530057A22 3', mRNA sequence.  
ACCESION BB219800.2 GI:16353450  
VERSION  
KEYWORDS  
SOURCE EST.  
ORGANISM house mouse.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 689)  
REFERENCE  
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanaaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyu,T., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)  
Unpublished (2001)  
On Jun 30, 2000 this sequence version replaced gi:8884753.  
Contact: Yoshinide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-resgsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/  
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Maitahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and



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OY      56  AAGGTGTGCTCGTGGACAGAGCTATCCAAAGTTTGGTTATGAGGA -GGGTGGAGT 114
Db      120  ACTGGTGTGCTCGTGGACAGAGCTATCCAAAGTTTGGTTATGAGGATGGGTGAGAT 179
OY      115  GCGTACTGACAGACCTGCTCCCTCCGAGGTACAAAAGAGTGGGCGCACCACTAATGT 174
Db      180  GCGTACTGACAGACCTGCTCCCTCCGAGGTACACAGAGCTGGGACACACAGATGT 239
OY      175  CAGAGTTGATCAGCTGTGCTGTATCAGTGTTCAGAGGTCAACTGTCACAG -CTAC 233
Db      240  CAGAGTTGATCAGCTGTGCTGTATCAGTGTTCAGAGGTCAACTGTCACAGCTTAC 299
OY      234  CTCTAATGCTGTGTGGGAGCTGTGGCCAGGTGTACCGAAAGACAGCATTTGAGG 293
Db      300  CTCTAATGCTGTGTGGGAGCTGTGGCCAGGTGTACCGAAAGACAGCATTTGAGG 359
OY      294  CCGTCAAGACC -AAGATGATCCCGTGCAGAACGACCCCACTGTGAGGTCAAT 352
Db      360  CCGTCAAGACCAGATGATCCCGTGCAGAACGACCCCACTGTGAGGTCAAT 419
OY      353  GTGCTTCCAGTTGA -GCTTAGTGA -GGCAGATGACCCAGTGGCCCTCAGAGGC 410
Db      420  GTGCTTCCAGTTGAGCTTAGTGATGAGATGACACCCAGTACCCCTCAGAGGC 479
OY      411  CACACTTGTGCACTGTGA -GCAGCTGC -TAGTGTGTTTACCTGCGCTTCTGCGG 468
Db      480  CACACTTGTGCACTGTGTGGAGAGCTGTGATGTGTGTTTACCTGCGCTTCTGCGG 539
OY      469  CTCTTCTCTCTACTGCAAGCTTCTTCA -ACAGACATTTGCCAGCGTGGAGGT -TT 524
Db      540  ATCTTCTCTCTACTGCAAGCTTCTTCAACACAGCTTGGCCAGAGCTGGAGTCTT 599
OY      525  GCTGAGTTTGAAGCTG -ATMAACAGCAAGAGGATCTCTCT 568
Db      600  GCTGAGTTTGAAGCTGATCAATAGCAAGAGGATATCT 644

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**RESULT 3**  
**BB627119**  
**LOCUS** BB627119 RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck Mus musculus CDNA clone  
**DEFINITION** 9430060422 5', mRNA sequence.  
**ACCESSION** BB627119  
**VERSION** BB627119.1 GI:16464896  
**KEYWORDS** EST.  
**SOURCE** house mouse.  
**ORGANISM** Mus musculus.

**REFERENCE** 1 (bases 1 to 697)  
**AUTHORS** Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hotchi,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M., and Hayashizaki,Y.  
**RIKEN Mouse ESTs** (Arakawa,T., et al. 2001)  
**COMMENT** Unpublished (2001)  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
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 Fax: 81-45-503-9216  
 Email: genome-resesc.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

M., Kono,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)  
 wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)  
 Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y., and Hayashizaki,Y.  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)  
 Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamamaki,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.  
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome.* 12, 673-677 (2001)  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.  
 e mouse tissues.

#### FEATURES

**source** Location/Qualifiers  
 1..697  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="943006042"  
 /clone\_1lb="RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck"  
 /tissue\_type="embryonic body between diaphragm region and neck"  
 /dev\_stage="12 days embryo"  
 /lab\_host="DH10B"  
 /note="Site.1: SalI; Site.2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 15'  
 GAGAGAGAGAGATCCAGAGCTCTTTTATTTTTTNN 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence 15' GAGAGAGAGATTCGAGTAAATTAATTAATCCCCCCCCC 3'. cDNA was cleaved with XhoI and BamHI."

**BASE COUNT** 184 a 166 c 172 g 175 t  
**ORIGIN**  
 Query Match 51.8%; Score 359.2; DB 9; Length 697;  
 Best local similarity 85.8%; Pred. No. 4.7e-91;  
 Matches 422; Conservative 0; Mismatches 68; Indels 2; Gaps 2;  
 OY 1 ATGATTTGCGCAAGAAATGACTATTGGACCAACTGGGAGCGGTGTGCACCTTGCCA 60  
 Db 182 ATGATTTGCGCAAGAAATGACTATTGGACCAACTGGGAGCGGTGTGCACCTTGCCA 241  
 OY 61 TGTGTCCTTGACAGAGAGCTATCCAAAGTTTGGTTATGAGAGGTGGAGATGCTTAC 120  
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 OY 121 TGCACAGCTGCGCTCTGTCAGTACAAAGAGCTGGGGGCCCAATGTCACAGT 180  
 Db 302 TGCATATGTCGCTCTGTCATCAATGCGGCCCAAGAGCTGTCACAGT 361  
 OY 181 TGCATACCTGTGCTGTATCAATGCTGTTCAGAGGTGTCACAGCTACTCTTAAT 240  
 Db 362 TGCATACCTGTGCTGTATCAATGCGGCCCAAGAGCTGTCACAGTACTCTTAAT 421

QY	241	GCTGTCGTGGGGACGTGTTTGCCAGGTTTCACGAAAGACACGATGGAGGCGCTGGAG	300
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QY	301	GACCAAGAGTGCATTCGCCGTGCACGAGACGACGCCACCTCTGAGGTTCAATTGTGCCCTTC	360
Db	482	GACCAAGAGATGCATTCGCCATGTATCAAAAGCAGACTCTCTTCCGAGGTTCAAGTGTACCTTC	541
QY	361	CAGTTGACCTTAGTGGAGGACGAGATGCACCCACGAGGCCGCCCTCAGAGGAGGCCACATTTGTT	420
Db	542	CAGTTGACCTTAGTGGAGGATGATGCACACACTGTTCCTCCCTTAGGGAAGCCACACTTTGTT	601
QY	421	GCATCTGCT-GAGCAGCCCTGCTAGTGTGTTTAAACCTTGACC-TTCCGTGGGCGCTCTTCTTCC	478
Db	602	GCACGTGGTGGGAAGTCTGTAGTGTATTGTCTGTGCGCTTCTCTTGAGACTCTCTCTCC	661
QY	479	TCTACTGCAGAC	490
Db	662	TTTATTGGAGAC	673

RESULT 4	
LOCUS	B651661
DEFINITION	B651661 680 bp mRNA linear EST 26-OCT-2001
	B651661 RIKEN full-length enriched, ES cells Mus musculus CDNA
	clone C330006C18 5', mRNA sequence.

ACCESSION	BB031001	
VERSION	BB651661.1	GI:16485901
KEYWORDS	EST,	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE  
AUTHORS

Arakawa, T., Carnicini, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hoti, F., Ishii, Y., Ito, M., Kawaji, J., Konno, H., Kouda, M., Koyu, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasakii, D., Shibata, K., Shinagawa, A., Shitlrick, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Tsurumatsu, M., and Hayashiki, Y.

TITLE	RIKEN Mouse ESTs (Arakawa, T., et al. 2001,
JOURNAL	Unpublished (2001)
COMMENT	Contact: Yoshinhide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
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Tel: 81-45-503-9222  
Fax: 81-45-503-9216

Email: [genome-res@sc.riken.go.jp](mailto:genome-res@sc.riken.go.jp),  
URL: <http://genome.gsc.riken.go.jp/>  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10): 1617-1630 (2000)

wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Iawa, M., Ohara, E., Matsubiki, M., Yoneda, Y., Ishikawa, T., Oawa, K., Tanaka, T., Matsuura, S., Kanai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771. (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Salto, I., Aiyosawa, H., Iamawaka, I., K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

# Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences. Mamm. genome. 12, 673-677 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.  
e mouse tissues.

FEATURES	Location/Qualifiers
source	1. .680

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clonetype="ES cells"

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/lab_host="SOLR"
/notes:Site_1: XhoI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',

```

GAGAGAGAGAGATCCAGACACTCTTTTTTTTTTTTTTTTVN 3'), cDNA was prepared by using thermostable thermophilic reverse transcriptase and subsequently enriched for full-length transcripts by using a 5' cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATCTCGAGTATTATTAATCCCTCCCTCCCC 3' ]. "

BASE COUNT	186 a	156 c	172 g	166 t
ORIGIN				

Query Match 47.3%; Score 327.8; DB 9; Length 680;

Best Local Similarity	82.9%;	Pred. No. 3.8e-83;		
Matches 374;	Conservative 0;	Mismatches 77;	Indels 0;	Gaps 0;

1 ATGGATTGCCAAGAAAATGAGTACTGTGGACCAATGGGGACGCGTGTGTCACTGCCACGG 60

Db 225 ATGATTTGTCACAGAGATGAGTACCGGACCAATGGGGGCGCTGTGTCACTGCCACAA 284

61 TGTGTCCTGGACAGGAGCTATCCAAAGCATTTGTGTTATGAGAGAGGTTGAGATGCTTAC 120

Db 285 TCTGGCCCTGACACGAGCCTCGAAGATTGTGTATATGGAGAAGTTGAGATGCACAC 344

121 TGCACAGCCTGGCCTCTTCGACAGGTACAAAAGCAGCTGGGGCCACACCAATGTCAGAGT 180

Db 345 TGCATAGTCTGCCCTCCCGGAAGTATPAAAGCACCTTGGGACATCACAGATGTCAGACA 404

181 TGCATCACCTGTGCTGTCATTCATCTGTTCAGAGCTCACTGCACAGCTACCTTAAT 240

Db 405 TGCATCAGCTTGGCTGTCATCAATCGGTCGAGAGGCCAATGCAACAATACCTCTAAT 466

241 GCTGTCGTGGGGAACCTGTTTGGCCAGGTTTACCCGAAGAAGACACGCAATTGGAGGGCCTGCAG 300

Db 465 GCATCTGTGGAGACTGTCTGTCCAGGCTTACCGAAAGACACGCCCTTGGGGGCTGCAG 524

301 GACCAAGAGTCATCCCGTGTGACGAAGACACCCCACTCTGAGCTTCAATGTGCCCTTC 366

Db 525 GACCAAGATGCATTCCATGTACAAAGCAGACTTCTTCTTCCGAGGTTCAAGGGTACTCT 584

361 CAGTTGACCTTAAGTGGAGGCGATGCACCCACAGTCCCCCTCAGAGGGCCACACTTGT 420

Db 585 CACCTTGAGCTTAGTGAAGCAGATGCACACTGTTCCTCCCTAAGGAAGCCACACTTGT 644

421 GCACTGGTGAGCAGCCTGCTACTGTTGTTTA 451

Db 645 GCACTGCGGGGGA6CCCTGCTGCGGGGTA 675

BB637179  
RESULT 5  
PB637170  
514 bp  
mpDNA  
linear  
EST 36-OCT  
TCCGTC

LOCUS	BB037179	014 bp	linear	EST	26	Oct	2003
DEFINITION	BB037179	R1EN	full-length enriched, adult male aorta and vein Mus musculus	cdna	clone	AF20057A22	5'

ACCESSION BB637179

BB637179

VERSION KEYWORDS	SOURCE	ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL COMMENT
B8637179.1 GI:16472964 EST.	house mouse. Mus musculus	Euryarchaea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1 (bases 1 to 614)	
			Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasakihara,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
			Unpublished (2001)	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216
			Email: genome-resgsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
			wagii,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsubara,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
			Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
			Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanae,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.	Computational Analysis of full-length mouse cDNAs compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
			Please visit our web site (http://genome.gsc.riken.go.jp) for further details.	
			e mouse tissues.	

			strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAAGATTCCTGAGTTAATTAAATTACCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda phage.	
			FIG. 1	
BASE COUNT	166 a	145 c	156 g	147 t
ORIGIN				
Query Match	42.0%	Score 291;	DB 9;	Length 614;
Best Local Similarity	85.9%;	Pred. No. 9.9e-72;		
Matches 346;	Conservative	0; Mismatches 55;	Indels 2;	Gaps 2;
OY	1	ANGGATTCGCCAAGAAATATGACTGTGGACCAACAATGGGACCGTGTGTCACCTCCACCACGG	60	
Db	1B2	ATGGATTTGCACGAATAATGATGATCCGGGGCCAATGGGGCGCTGTCTCACCTCCGCAACAAA	241	
OY	61	TGTGTCCTCGACAGAGAGCTATCCAAAGCATTTGTGGTTATGAGAGGAGTGAGATCGCTTAC	120	
Db	242	TGTGGCCCTCGACAGAGAGCTCTCGAAGGATTTGTGTATGAGAAAGTGTGAGATCAGAAC	301	
OY	121	TGCACAGCCCTGGCCCTTCCTGCAGGTACAAAAAGACAGCTGGGGCCACCAAATGTCCAGAT	180	
Db	302	TGCATATGCTCGCCCCTCCGCCGAAAGATATAAAGCACCTTGGGAGCATACAGATGTCAGACA	361	
OY	1B1	TGCATCACCTGTGCTGTATCATCATGTGTTCGAAAGGTCACTGCACAGCTTACTTAT	240	
Db	362	TGCATCACTTGTGCTGTATCATCATGGGTGCCAAGGGCCAACTGCACAAATACCTCTAAT	421	
OY	241	GCTGTCTGTGGGAGCTGTGGCCAGGTTCCTACGAAAGACACGCAATTTGGAGCGCTCGAG	300	
Db	422	GCTATCTGTGAGACTGTCTCTGCCAGGTTTCTTACGAAAGACACGCAATTTGGGGCGCTCGAG	481	
OY	301	GACCAAGAGTGCATCCGTGCACGAGACGAGACCCCACTGTGAGTTTCAATGTGCC--TT	359	
Db	4B2	GACCAAGATGATGCCATGTCACAAAGAGAGACTCTTCTTCGAGAGTTTAGTGATCTTT	541	
OY	360	CCAGTTGAGCTTAGTGG+AGCGACATGCACCCACAGTSCCCCC	401	
Db	542	CCAGTTGAGCTTAGTGGAGAGTATGCACACACTGTGTCC	584	
RESULT 6				
BBS58916				
LOCUS	BBS58916	459 bp	mRNA	linear EST 26-NOV-2001
DEFINITION	BBS58916 RIKEN full-length enriched, kidney CCL-142 RAG CDNA Mus musculus cDNA clone GA30003D23 5', mRNA sequence.			
ACCESSION	BBS58916			
VERSION	BBS58916.1	GI:17100370		
KEYWORDS	EST.			
SOURCE	Mus mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus. 1 (bases 1 to 459)			
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TITLE	Unpublished (2001)			
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